

WHAT IS CLAIMED IS:

1. A data processing system for managing and presenting information derived from a differential expression of genetic information which can be used to model a physiological response of biological cells, said system comprising:

a data-represented map of metabolic pathways, said map having a matrix of regions and locations within each said region, said regions being defined by respective coordinate sets, each of said metabolic pathways comprising at certain ones of said locations respective graphical representations of a reaction, a substrate and a product of the reaction, and at least one biological catalyst of the reaction; and

an association mechanism which links previously generated sets of affected sequence data to biological catalyst identifiers each identifying one or more unique biological catalysts, and which links said biological catalyst identifiers to said coordinate sets, said sets of affected sequence data representing a direction and a magnitude of regulation of each one of a number of different nucleic acid sequences.

2. The data processing system of claim 1 further comprising:

a grading mechanism which assigns a corresponding grade to a corresponding region in accordance with a number of said sets of affected sequence data linked to said corresponding region by said association mechanism.

3. The data processing system of claim 2 further comprising:

a display mechanism for displaying an overview of said map and a detailed view of said map, said overview graphically representing said regions of said map and said corresponding grades, and said detailed view comprising detailed graphical representations of said metabolic pathways comprising affected biological catalyst indications of locations of those of said biographical catalysts corresponding to said sets of affected sequence data, each said affected biological catalyst indication representing a direction of regulation of the set of affected sequence data corresponding thereto.

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4. A method of managing and presenting information derived from a differential expression of genetic information which can be used to model a physiological response of biological cells, said method comprising:

providing a data-represented map of metabolic pathways, said map having a matrix of regions and locations within each said region, said regions being defined by respective coordinate sets, each of said metabolic pathways comprising at certain ones of said locations respective graphical representations of a reaction, a substrate and a product of the reaction, and at least one biological catalyst of the reaction; and

linking sets of previously generated affected sequence data to biological catalyst identifiers each identifying one or more unique biological catalysts, and which links said biological catalyst identifiers to said coordinate sets, said sets of affected sequence data representing a direction and a magnitude of regulation of each one of a number of different nucleic acid sequences.

5. The method of claim 4 further comprising:

assigning a corresponding grade to a corresponding region in accordance with a number of said sets of affected sequence data linked to said corresponding region by said linking.

6. The method of claim 5 further comprising:

displaying an overview of said map and a detailed view of said map, said overview graphically representing said regions of said map and said corresponding grades, and said detailed view comprising detailed graphical representations of said metabolic pathways comprising affected biological catalyst indications of locations of those of said biological catalysts corresponding to said sets of affected sequence data, each said affected biological catalyst indication representing a direction of regulation of the set of affected sequence data corresponding thereto.

7. A machine-readable medium having data recorded thereon such that when the data is read into a computer and executed, the data causes the computer to:

use a data-represented map of metabolic pathways, said map having a matrix of regions and locations within each said region, said regions being defined by respective

coordinate sets, each of said metabolic pathways comprising at certain ones of said locations respective graphical representations of a reaction, a substrate and a product of the reaction, and at least one biological catalyst of the reaction; and

link sets of previously generated affected sequence data to biological catalyst identifiers each identifying one or more unique biological catalysts, and which links said biological catalyst identifiers to said coordinate sets, said sets of affected sequence data representing a direction and a magnitude of regulation of each one of a number of different nucleic acid sequences.

8. The machine-readable medium of claim 7, wherein said data further causes the computer to:

assign a corresponding grade to a corresponding region in accordance with a number of said sets of affected sequence data linked to said corresponding region by said linking.

9. The machine-readable medium of claim 8, wherein said data further causes the computer to:

display an overview of said map and a detailed view of said map, said overview graphically representing said regions of said map and said corresponding grades, and said detailed view comprising detailed graphical representations of said metabolic pathways comprising affected biological catalyst indications of locations of those of said biographical catalysts corresponding to said sets of affected sequence data, each said affected biological catalyst indication representing a direction of regulation of the set of affected sequence data corresponding thereto.